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BLUP Estimation and Genotype Stability in *Arachis hypogaea* L. Variety Testing using Mixed Model Equations

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ABSTRACT

Background: One of the major goals of plant breeding is the selection of high yielding superior cultivars having wide or specific adaptation. However, there is a fluctuation in the annual production due to the sensitive behaviour of the genotypes under different environmental conditions referred to as Genotype by Environment Interaction (GEI). The current study aimed to study the contribution of GEI for the adaptation of groundnut lines for spring and/or *kharif* season.

Methods: To assess the contribution of GEI, Multi-Environment Trials (METs) were conducted for 40 confectionery purpose groundnut genotypes at F_9 generation along with checks, across three locations for two seasons (spring and *kharif*). The contribution of environmental effects, genotypic values and genotype × environment interaction values were obtained from genotypic variance-covariance matrix $Gi = \Sigma_g \otimes A$ using mixed models (MM) in Best linear unbiased predictions (BLUPs).The pooled data was first partitioned into fixed effects of sites across the seasons and BLUP genotypic values (G*gge*). The BLUP genotypic values are further partitioned into genetic value (G*g*) and their interaction with the environment (G*ge*) for the adaptability of genotypes across seasons.

Result: The results of MET revealed the presence of significant crossover interaction. The demarcation of advance breeding lines for adaptability across the environment as well as for season specific adaptation was done for variety testing. Genotypes having moderate to high G*ge* values along with high G*g* values in spring than *kharif*, owing to their better performance during the spring season. CGL-11, CGL-23 and CGL-04 were the highest yielding genotypes, with quite high G*ge* values. This is due to the more favourable environmental conditions interacting positively with genotypes during the spring. Thus, the high G*g* value(s) of genotype(s) alone is not a capable factor for commercialization as G*ge* value is the deciding factor for the adaptability for the targeted season.

Key words: BLUPs, Genetic effect, Genotypic value, Groundnut, Mixed model.

INTRODUCTION

Domesticated groundnut (*Arachis hypogaea* L.) is an important self-pollinating, tropical legume mainly grown for oil production in more than 100 countries. Asia is the major groundnut producing region with China being the major contributor (17.39 million tons) followed by India (6.6 million tons) (FAOSTAT, 2018). However, there is a fluctuation in the annual production due to the sensitive behaviour of the genotypes to different environmental conditions (Mekontchou *et al*., 2006), referred as Genotype by Environment Interaction (GEI). Since, in plant breeding, high yield is a major goal, it is important to select superior cultivars having wide or specific adaptation, which can be tested by its degree of interaction with different environments (Hardwick *et al*., 1972; Finlay and Wilkinson, 1963). For this, Multi-Environment Trials (METs) can be used, which provide an estimate of the overall stability and adaptability of the genotype(s), along with GEI. The statistical models developed earlier, for studying GEI were based on the two-way fixed-effects or random-effects models (Cornelius *et al*. 1996; Cornelius and Crossa, 1999) assuming sites to be independent considering the pairwise covariances between sites be zero and variances within sites, be equal (Crossa *et al*., 2001; Cornelius *et al*., 2001). These models further assume the spatial independence of individual field plot errors in each site and the genotypes to be unrelated. However, these assumptions are not realistic as related genotypes i.e., full-sibs, half-sibs, sister lines tend to be more alike than unrelated genotypes. As a result, more complex and informative mixed linear models have been proposed for efficient data analysis. Linear model underlying Best Linear Unbiased Predictors (BLUP) and best linear unbiased estimates (BLUE) is called mixed model because it includes both fixed and random effects. The various advantages associated with these models involve efficient handling of unbalanced or incomplete data, *i.e*., not all lines or genotypes are tested in all environments, ability to assume some effects for example, variety and/or environment to be random than as fixed effect (Smith *et al.,* 2005).

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The general linear mixed model can easily accommodate covariances among observations. The mixed model handles correlated data by incorporating random effects and estimating their associated variance components to model variability over and above the residual error (Wolfinger and Tobias, 1998). Mixed models assume some effects to have arisen from the distribution of random-effects, implying the presence of a broad population of genetic effects and the samples being the realized values from that population, which can be predicted by BLUPs (Henderson, 1975). The analysis of metric data based on mixed linear model can be of the form.

$$y = X\beta + Z\mu + e$$

Where,
y = Vector of observations.
β and μ = Vectors of fixed and random effects, respectively.
X and Z = Associated design matrices.
e = Residual vector.

The random effects are assumed to have a distribution as u ~ *MNV* (0, G) and e ~ *MNV* (0, R) with *MNV* as multivariate normal distribution with mean vector μ and variance co-variance matrix V (Piepho *et al*., 2008). For variety testing and development of new varieties genotype effects are often considered as fixed effects thus becoming a part of â in the mixed model. But, when genotypes are considered to be random effects, the genotypic effects become a part of u and thus, estimated by BLUP. Smith *et al*. (2005) argued that genotype effects should be specified as random in a statistical mixed model because this: (1) minimizes selection errors when identifying the best genotypes, (2) provides more realistic estimates of genotype performance (predictions of genetic gain) and (3) allows a valid analysis of data combined across stages/generations of selection. The choice to classify variety effects as fixed or random depends upon the aim and the properties of the two estimation procedures *i.e*., empirical best linear unbiased prediction (E-BLUP) for random effects and best linear unbiased estimates (E-BLUE) for fixed effects considered for the analysis (Smith *et al.,* 2005). If the analysis aims to identify the best variety out of those under consideration, then, the variety effect should be considered random, implying the use of BLUPs during the early stages of the selection program. However, the same can be considered as a fixed effect at later stages of selection or, if the aim is to determine the difference between specific pair of varieties, as BLUP of a specific difference is biased and hence will be inappropriate to use (Federer 1997; Smith *et al.,* 2005). When, genotypic main effects are taken as random the mixed model can be defined as:

$$\mu_{ij} = \mu + G_i + E_j + \varepsilon_{ij}$$

$$G_i \sim N(0, \sigma^2_G) \text{ and } \varepsilon_{ij} \sim N(0, \sigma^2_\varepsilon)$$

The model has two variance components, one corresponding to the random genotypic main effects (σ^2_G) and the other *i.e*., σ^2_ε corresponding to the residual, that involves true GEI and error (Malosetti *et al*., 2013).

In plant breeding, a breeder as to make selection among a large set of candidate genotypes and thus, it is important to make phenotypic selection based on the estimated genotypic values for varietal testing and commercialization (Piepho *et al*., 2008). BLUPs can serve as a great tool to select the best individuals as it maximizes the correlation of true genotypic values and the predicted genotypic values (Searle *et al*., 1992). Hence, in the present investigation, the phenotypic values are partitioned into genetic value (G*g*) and their interaction with environments (G*ge*) using mixed model equations (MME) in BLUPs as suggested by Crossa *et al.* (2006) including co-ancestry of parents (COP) to elucidate precise estimates of genetic values vis-à-vis their environmental interactions.

MATERIALS AND METHODS

Experimental material: Due to high marketing avenues and mounting demand of table purpose groundnut, Punjab Agricultural University, Ludhiana geared up research programme to breed for confectionery groundnut since 2011-12. Under this program, advanced breeding material was generated through pedigree breeding method using the parental lines developed by The International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India (ICGV series), Bhaba Atomic Research Centre (BARC), Trombay (TG-lines) and various state agricultural universities such as GJG- and GG-lines from Junagadh Agricultural University (JAU), Junagadh, DH-lines from University of Agricultural Sciences (UAS)Dharwad. From this material, a set of 40 advanced breeding lines (ABL) at F_9 generation, comprising full sibs (having the same male and female parents) and half sibs (individuals that have one parent in common) were used in the present study (Table 1).

Experimental design

Three released varieties J-87, SG-99 and TG-37A were used along these test lines as checks. The test genotypes were planted in the alpha lattice design with three replications each. A plot of three rows of three-meter-length were sown for each genotype with row-to-row and plant-to-plant spacing of 30 cm and 15 cm, respectively in each replication. The lines were grown across three locations in Punjab state of India *viz*., Ludhiana, Kheri and Kapurthala for two seasons spring (mid-March to June) and *kharif* (first fortnight of July to October). The *kharif* season (main crop season) accounts for about 80% of the total groundnut production (Vijaya, 2007). Monsoon variations cause major fluctuations in groundnut production in India. Groundnut is grown in different cropping systems like sequential, multiple and intercropping (Basu and Ghosh, 1995). If irrigation facilities are available and fits in cropping pattern, groundnut can be grown during January to May as a spring or summer crop as well. Spring cultivation of groundnut is taken in the states of Uttar Pradesh, Punjab and West Bengal etc. (March to May). The two seasons vary in their weather parameters such as temperature, humidity and rainfall (Table 2a,b). Abiotic stresses such as variation in rainfall (Sindagi and Reddi, 1972) are prevalent during spring season. While, biotic stresses are such as disease incidences are prevalent during *kharif* season giving differential response of genotypes with diverse genetic background.

Statistical analysis

The variance-covariance matrix of additive genetic effect was obtained from COP multiplied by the population additive genetic variance, σ_a^2. Genotypic values and genotypic × environment interaction was obtained from genotypic variance-covariance matrix $Gi = \Sigma_g \otimes A$ using mixed models (MM) in BLUPs as suggested by Crossa *et al*. (2006) *i.e*.,

$$Gi = \Sigma_g \otimes A = \begin{bmatrix} \sigma_{a_1}^2 & \rho_{12}\sigma_{a_1}\sigma_{a_2} & . & . & . & \rho_{1s}\sigma_{a_1}\sigma_{a_s} \\ \rho_{12}\sigma_{a_1}\sigma_{a_2} & \sigma_{a_2}^2 & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ \rho_{1s}\sigma_{a_s}\sigma_{a_1} & . & . & . & . & \sigma_{a_s}^2 \end{bmatrix} \otimes A$$

Variance-covariance matrices R and N are assumed to have a simple variance component structure, as defined for MME.

$$R = \Sigma_r \otimes I_r = \quad I_r = \begin{bmatrix} \sigma_{r_1}^2 & 0 & . & . & . & 0 \\ 0 & \sigma_{r_2}^2 & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ 0 & . & . & . & . & \sigma_{r_s}^2 \end{bmatrix} \otimes I_r, \text{ and}$$

$$E = \Sigma_e \otimes I_{rg} = \begin{bmatrix} \sigma_{e_1}^2 & 0 & . & . & . & 0 \\ 0 & \sigma_{e_2}^2 & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ . & . & . & . & . & . \\ 0 & . & . & . & . & \sigma_{e_s}^2 \end{bmatrix} \otimes I_{rg},$$

Where,

I_r and I_{rg} = Identity matrices of orders r and rg, respectively,

Σ_r and Σ_e = Replicate and residual variance matrices, respectively.

$\otimes$ = Kronecker (or direct) product operator.

The unstructured variance-covariances are transformed to heterogeneity of within environment genetic variance (CSH model), in which case Σ_{gi} or Σ_{ge} has structure:

$$\{diag(\sigma_{aj}) [(1 - \rho) I_s + \rho J_s] \, diag(\sigma_{aj})\} \otimes A$$

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance (ANOVA) (Table 3) was performed to determine the significance of genotypes, environments and their interaction effect on the performance of the given

Table 1: List of the advanced breeding lines (ABL) of groundnut used for evaluation in Multi-Environment Trial (MET).

ABL	Pedigree
CGL-01	(M-522 × M-13)-F_1-F_2-1-2-3-1-B
CGL-02	(M-522 × M-13)-F_1-F_2-1-2-5-2-B
CGL-03	(M-522 × M-13)-F_1-F_2-6-4-3-1-B
CGL-04	(M-522 × M-13)-F_1-F_2-7-4-3-2-B
CGL-07	(M-522 × BAU-13)-F_1-F_2-1-1-3-2-B
CGL-08	(M-522 × BAU-13)-F_1-F_2-1-8-6-2-B
CGL-11	(M-522 × BAU-13)-F_1-F_2-11-4-3-2-B
CGL-13	(M-522 × BAU-13)-F_1-F_2-15-1-8-7-B
CGL-14	Mutant of M-522-M_2-2-3-B
CGL-20	Mutant of M-522-M_2-2-10-B
CGL-22	Mutant of M-522-M_2-8-4-1-B
CGL-23	Mutant of M-522-M_2-9-3-B
CGL-27	(PBS-29078 × ICGV-00440)-F_7-1-B
CGL-29	(PBS-29078 × ICGV-00440)-F_7-9-B
CGL-33	(ICGV-97079 × GG-20)-F_6-1-1-B
CGL-35	(ICGV-97079 × GG-20)-F_6-1-6-B
CGL-36	(ICGV-97079 × GG-20)-F_6-1-2-B
CGL-37	(ICGV-97079 × GG-2)-F_6-1-6-B
CGL-39	(ICGV-97079 × GG-2)-F_6-2-1-B
CGL-40	(ICGV-97079 × GG-2)-F_6-2-7-B
CGL-46	(TG-40 × ICGV-97079)-F_6-1-1-B
CGL-48	(ICGV-97097 × DH-3-30)-F_5-2-2-1-B
CGL-49	(ICGV-97097 × DH-3-30) -F_5-2-2-8-B
CGL-50	(ICGV-97097 × DH-3-30) -F_5-4-1-2-B
CGL-53	(ICGV-97097 × DH-3-30)-F_5-12-1-13-B
CGL-58	(ICGV-97079 × MH-4)-F_5-1-1-4-B
CGL-61	(ICGV-97079 × MH-4)-F_5-1-1-4-B
CGL-62	(ICGV97079 × MH-4)-F_5-1-4-4-B
CGL-63	(ICGV97079 × MH-4)-F_5-7-2-3-B
M-13	Selection from 'NC-13'
M-522	PG-1 × F334-AB-14
GJG (HPS-1)	JSP-21 × VG-5
J-87	-
Raj mig-3	-
Mallika	(ICGV-88386 × ASHFORD) × ICGV-95172-F_2-B1-B1-B3-B1
SG-99	ICGV-86829 × ICGV-87160 {ICG(FDRS)-10}
TG-37A	TG-25 × TG-26
M-548	M-37 × Blanco Puro White
TAG-24	Selection from TGS-2 (TG-18A × M-13) × TGE-1 (Tall mutant × TG-9)
Gangapuri	Selection from local strain

groundnut genotypes for the test traits: pod yield (kg/ha), pods per plant, shelling percentage, seeds per pod, sound mature kernels, 100 seed weight (g) and oil % under different crop durations *i.e*., spring and *kharif*. The combined analysis of variance showed the significant GEI, depicting the influence of environment on the test genotypes in terms of their response to agronomically important traits.

Mean yield performance of genotypes

The mean yield of the genotypes is presented in Table 4. The mean yield of genotypes ranged from 4509 kg/ha (CGL-23) to 1784 kg/ha-(CGL-63) and 3474 kg/ha (CGL-22) to 1255 kg/ha (CGL-63) during *kharif* season. The five top ranked lines for pod yield wereCGL-23 (4509 kg/ha) CGL-11 (4491 kg/ha), J-87 (4423 kg/ha), CGL-22 (4291 kg/ha) and CGL-50 (4193 kg/ha) during spring season. CGL-22 (3474 kg/ha) followed by CGL-23 (3336 kg/ha), J-87 (3199 kg/ha), Mallika (3141 kg/ha) and CGL-11 (3138 kg/ha), was highest yielding during *kharif* season. Genotypes M-13, Gangapuri, CGL-46 and CGL-63 had consistently low yield performance during both the seasons. All the genotypes had overall 36.87% higher productivity in the spring sown crop than, *kharif.* This variability in the yield reflects the overall influence of environmental conditions during growing seasons such as temperature, relative humidity and disease pressure. Thus, selection of genotypes based on their phenotypic performance alone may hinder varietal selection and recommendation, as it is not known whether the genotype or the environment is responsible for the interaction causing a change in the genotypic ranking.

Stability analysis

For estimating the adaptability of genotypes, the pooled data was partitioned into fixed effects of sites across seasons and BLUP genotypic values (G*gge*). The BLUP genotypic values are further partitioned into genetic value (G*g*) and their interaction with the environment (G*ge*) to assess the adaptability of genotypes across seasons (Table 5). The ranking of top ten genotypes based on their pooled G*g* values is CGL-22 followed by CGL-04, CGL-36,

Table 2a: Weather parameters during spring (2019) for: Temperature (°C), Relative Humidity (RH%) and Rainfall (mm).

Month	Temperature (°C)			Relative humidity (RH%)			Rainfall
	Maximum	Minimum	Mean	M	E	Mean	(mm)
March	25	12	19	89	46	67	7
April	35	20	27	71	30	50	42
May	38	22	30	52	22	37	10
June	40	27	34	55	30	42	30
Average	35	20	27	67	32	49	89

(Source: Department of Climate Change and Agricultural Meteorology, Punjab Agricultural University, Ludhiana).

Table 2b: Weather parameters during *kharif* (2019) for: Temperature (°C), Relative Humidity (RH%) and Rainfall (mm).

Month	Temperature (°C)			Relative humidity (RH%)			Rainfall
	Maximum	Minimum	Mean	M	E	Mean	(mm)
July	34	27	30	29	29	29	218
August	40	27	34	55	30	42	30
September	33	26	29	86	68	77	265
October	31	18	24	90	46	68	0
Average	34.5	24.5	29.25	65	43.25	54	513

(Source: Department of Climate Change & Agricultural Meteorology, Punjab Agricultural University, Ludhiana).

Table 3: Combined analysis of variance across six environments for the test characters of the groundnut test genotypes.

Characteristics		Pods per plant	Pod yield (kg/ha)	Shelling %	Seeds per pod	Sound mature kernels	100 seed weight (g)	Oil %
Source	df	Mean sum of squares						
Replication	12	4.05	0.04	11.71	0.01	16.96	36.79	2.38
Genotypes	39	351.25**	8.25**	206.81**	0.61**	1324.88**	1059.50**	24.29**
Environment	5	171.48**	26.75**	346.43**	0.01**	523.12**	1131.29**	151.07**
Genotype × Environment	195	11.32**	0.16**	74.26**	0.02**	41.18**	141.49**	6.10**
Error	468	2.42	0.11	5.11	0.002	8.12	14.50	1.01

** significant at 0.01% level of probability

CGL-23, J-87, TG-37A, CGL-53, M-548, CGL-14 and Mallika, but this ranking differs from the ranking with respect to G*gge* values (Table 5). Genotype CGL-23 has the highest G*gge* value followed by CGL-22 and CGL-11. Although CGL-22 ranks 2 with respect to G*gge* but ranks 1 with respect to G*g* value with low G*ge* value, thus performance of the line is not much affected by the environment, implying the genotype is the main contributing factor for the yield performance. Further, CGL-23 having the highest G*gge* value (rank 1) but has low G*g* value (rank 4) with quite high G*ge*, implying environment has a significant contribution for the yield performance of the genotype. Similarly,

Table 4: Mean pod yield (kg/ha) of 40 advanced breeding lines of groundnut along with the checks at three locations across seasons: Spring and *kharif* three locations.

Genotype	Spring			Mean		*Kharif*			Mean	
	Ludhiana	Kheri	Kapurthala			Ludhiana	Kheri	Kapurthala		
CGL-01	3655	3973	2702	3443	16	2566	2551	2057	2391	18
CGL-02	2724	2922	3625	3090	20	2136	2482	2211	2276	22
CGL-03	2869	3002	3058	2976	22	1987	1975	2656	2206	24
CGL-04	3731	4154	3701	3862	8	2919	2902	2879	2900	7
CGL-07	3331	3258	3304	3298	18	2580	2565	2352	2499	15
CGL-08	2901	3576	2879	3119	19	2253	2240	2326	2273	23
CGL-11	4359	4790	4324	4491	2	3103	3289	3022	3138	5
CGL-13	2860	3400	2842	3034	21	2341	2331	2400	2357	20
CGL-14	3572	3793	3553	3639	11	2768	2544	2820	2711	12
CGL-20	3280	3501	3258	3346	17	2196	2185	1763	2048	26
CGL-22	4244	4495	4134	4291	4	3423	3482	3516	3474	1
CGL-23	4231	4850	4446	4509	1	3403	3084	3522	3336	2
CGL-27	2751	2966	2567	2761	26	2435	2212	2446	2364	19
CGL-29	2314	2773	2296	2461	32	1516	1507	1500	1508	36
CGL-33	2695	2946	2673	2771	25	2378	2364	2461	2401	17
CGL-35	3547	3822	3518	3629	15	3024	3006	3130	3053	6
CGL-36	2494	2495	2475	2488	30	2077	2066	2048	2064	25
CGL-37	3630	3952	3598	3727	9	2811	2645	2921	2792	10
CGL-39	2622	2829	2253	2568	29	1724	1712	1895	1777	29
CGL-40	2096	2371	2075	2181	37	1543	1531	1617	1563	33
CGL-46	1785	1914	1771	1823	39	1264	1257	1310	1277	39
CGL-48	2331	2590	2307	2409	33	1330	1318	1888	1512	35
CGL-49	3677	4333	3647	3886	7	2717	2834	2812	2788	11
CGL-50	4292	4028	4258	4193	5	2587	2572	2678	2612	14
CGL-53	2853	3101	2830	2928	24	2405	2391	2489	2428	16
CGL-58	2276	2522	2258	2352	34	1519	1509	1572	1533	34
CGL-61	2679	3497	2658	2945	23	1985	1973	2054	2004	27
CGL-62	2564	2798	2543	2635	28	1840	1829	1527	1732	30
CGL-63	1638	1912	1802	1784	40	1243	1236	1287	1255	40
M-13	2034	2257	2369	2220	36	1386	1688	1435	1503	37
M -522	2175	2271	2531	2326	35	1623	1303	1979	1635	31
GJG(HPS-1)	2591	2681	2717	2663	27	1389	1685	1828	1634	32
J-87	4332	4641	4295	4423	3	3165	3143	3289	3199	3
Raj-Mig 3	2403	2612	2384	2466	31	2046	2033	1757	1945	28
Mallika	3593	3667	3340	3533	13	2975	3259	3190	3141	4
SG-99	3971	4317	3865	4051	6	2612	2597	2704	2637	13
TG-37A	3655	3860	3637	3717	10	2712	3151	2760	2874	8
M-548	3433	3679	3406	3506	14	3073	2308	3181	2854	9
TAG-24	3403	3706	3376	3495	15	2309	2295	2389	2331	21
Gangapuri	2038	1997	2024	2020	38	1456	1440	1136	1344	38
Mean	3041	3306	3033	3127		2270	2262	2320	2284	

(Values in the bold depict the ranking of the genotypes with respect to their mean yield during spring and *kharif* season).

genotype CGL-11 has high G*ge* value with low G*g* value but overall, third highest G*gge* value. Thus, these genotypes are adapted to particular season or environmental conditions. Certain genotypes such as CGL-01, CGL-02, CGL-03, CGL-08, CGL-20, CGL-27, CGL-35, CGL-37, CGL-46 CGL-48, CGL-50, CGL-58, CGL-61, CGL-62 had negative G*g* values, hence, these genotypes will contribute poorly for their overall yield even if environmental conditions contribute positively for the yield. J-87 (G*g*=524 kg/ha, G*ge*=1064 and G*gge*=1588) which was used as a

Table 5: Pooled Genetic values (G*g*), genetic value-by-environment interaction (G*ge*) and BLUP genotypic values (G*gge*) for the advance breeding lines of groundnut.

Genotype	G*g*		G*ge*	G*gge*	
CGL-01	-327	25	1001	675	17
CGL-02	-357	26	797	440	22
CGL-03	-235	22	599	364	24
CGL-04	778	2	438	1216	5
CGL-07	225	12	454	679	16
CGL-08	-214	21	678	464	21
CGL-11	247	11	1359	1606	3
CGL-13	5	15	462	467	20
CGL-14	439	7	538	977	10
CGL-20	-670	35	1138	468	19
CGL-22	1108	1	542	1650	2
CGL-23	718	4	989	1707	1
CGL-27	-664	33	761	97	27
CGL-29	-459	29	309	-149	32
CGL-33	126	14	209	335	25
CGL-35	-65	18	1000	935	13
CGL-36	733	3	-354	379	23
CGL-37	-28	16	996	968	11
CGL-39	-391	27	364	-27	29
CGL-40	-50	17	-190	-241	34
CGL-46	-612	32	4	-608	40
CGL-48	-946	40	687	-260	35
CGL-49	150	13	977	1128	7
CGL-50	-118	19	1290	1172	6
CGL-53	374	8	115	489	18
CGL-58	-680	37	419	-261	36
CGL-61	-666	34	892	226	26
CGL-62	-747	38	698	-48	30
CGL-63	-439	28	-158	-597	39
M-13	-585	30	255	-330	37
M -522	-676	36	442	-234	33
GJG(HPS-1)	-806	39	745	-61	31
J-87	524	5	1064	1588	4
Raj-Mig 3	-196	20	195	-1	28
Mallika	262	10	642	904	14
SG-99	-288	24	1414	1126	8
TG-37A	446	6	622	1068	9
M-548	371	9	582	953	12
TAG-24	-263	23	950	686	15
Gangapuri	-599	31	101	-499	38
Mean	-114		601	486	
Overall fixed environmental effects			2219		

The values in the bold depict the ranking of the genotype for their genetic value and BLUP genotypic values.

check had overall rank 4 for G*gge* value and rank 5 for G*g* value. The line had quite high G*ge* value indicating the significant contribution of the environmental effects for the yield, thus is adapted to particular season.

Table 6 represents the genetic values (G*g*), genotype-environment interaction (G*ge*) values and BLUP (G*gge*) genotypic values of lines across the seasons. During spring, genotype CGL-11, followed by CGL-23, CGL-04, CGL-22 and CGL-50 had the highest G*gge* value. During *kharif,* CGL-04, followed by CGL-23, CGL-11, CGL-22 and TG-37A had the highest G*gge*. On partitioning of G*gge* value,

Table 6: Genetic values (G*g*), genetic value-by-environment interaction (G*ge*) and BLUP genotypic values (G*gge*) for advanced breeding lines of groundnut.

Genotype	Spring					*Kharif*				
	G*g*		G*ge*	G*gge*		G*g*		G*ge*	G*gge*	
CGL-01	248	13	738	986	11	-57	14	-279	-336	26
CGL-02	-811	38	837	26	28	-1092	39	646	-446	27
CGL-03	-277	26	546	269	22	-339	22	214	-125	20
CGL-04	1439	1	155	1594	4	2129	1	-621	1508	1
CGL-07	273	11	410	683	17	145	8	91	236	13
CGL-08	-265	25	692	426	19	-678	29	438	-240	22
CGL-11	543	6	1393	1936	1	107	9	835	942	3
CGL-13	-92	22	456	363	21	-481	25	339	-141	21
CGL-14	591	5	495	1087	9	371	4	128	499	7
CGL-20	-440	29	1157	716	15	-839	34	580	-259	24
CGL-22	868	3	685	1552	5	-225	18	816	590	5
CGL-23	900	2	962	1862	2	750	2	470	1220	2
CGL-27	-720	37	468	-252	35	-818	33	321	-497	30
CGL-29	-353	27	385	32	27	-616	27	41	-574	31
CGL-33	103	17	85	188	25	32	11	38	70	17
CGL-35	97	18	605	702	16	-18	13	385	366	10
CGL-36	162	14	-42	120	26	22	12	-49	-27	18
CGL-37	-176	23	1015	839	13	-543	26	635	92	16
CGL-39	133	15	119	252	23	-92	16	-164	-256	23
CGL-40	-71	21	-104	-175	32	-270	19	-193	-463	28
CGL-46	-571	31	-29	-600	40	-625	28	-147	-772	37
CGL-48	-813	39	619	-194	33	-1069	38	261	-808	39
CGL-49	353	8	930	1282	8	78	10	410	488	9
CGL-50	267	12	1278	1545	6	-71	15	290	218	15
CGL-53	326	10	82	408	20	331	5	-61	270	12
CGL-58	-626	33	397	-228	34	-802	32	91	-711	35
CGL-61	-598	32	840	242	24	-879	35	411	-468	29
CGL-62	-667	35	648	-19	30	-902	36	278	-625	32
CGL-63	-424	28	-162	-587	39	-473	24	-225	-698	34
M-13	-655	34	224	-431	36	-771	31	40	-731	36
M -522	-917	40	473	-444	37	-1275	40	392	-882	40
GJG(HPS-1)	-686	36	708	22	29	-927	37	281	-647	33
J-87	778	4	1014	1792	3	409	3	443	852	4
Raj-Mig 3	-252	24	151	-102	31	-305	20	8	-297	25
Mallika	43	19	466	510	18	-113	17	333	220	14
SG-99	117	16	1342	1459	7	-314	21	625	311	11
TG-37A	484	7	585	1069	10	264	6	254	518	6
M-548	331	9	537	868	12	256	7	240	495	8
TAG-24	-67	20	905	838	14	-461	23	391	-70	19
Gangapuri	-566	30	79	-487	38	-698	30	-85	-783	38
Mean	-114		601	486		-50		554	504	
Fixed effects			2626					2333		

The values in the bold depict the ranking of the genotype for their genetic value and BLUP genotypic values.

CGL-04 had the highest G*g* value (rank 1) during both season but, low and positive G*ge* during spring and negative G*ge* during *kharif.* This positive G*ge* is responsible for the high yield of CGL-04 during the spring season than *kharif.* Similarly, although genotype CGL-23 has rank 2 during both the seasons, but there is a significant difference on the G*gge* values: 1862 kg/ha and 1220 kg/ha during spring and *kharif,* respectively. The genotype has high G*g* and G*ge* value during the spring than *kharif,* thus, environment is a major contributing factor for the high yield of the genotype during spring. Similarly, other top-ranking genotypes with respect to their yield performance CGL-22, CGL-50, SG-99, CGL-49 and CGL-14 were found to be more adapted to spring season. Thus, spring is more favourable growing season as depicted from overall higher fixed effects (2626 kg/ha) than *kharif* (2333 kg/ha). These, results are in agreement with the released check variety J-87 which has been released for the spring season by Punjab Agricultural University, Ludhiana, Punjab in 2020 for commercial cultivation. J-87 had similar rank during both seasons, but with large difference in the G*gge* value 1792 kg/ha and 852 kg/ha during spring and *kharif,* respectively. This variety had high G*g*=778 kg/ha and G*ge*=1014 kg/ha value during spring season, but low G*g*=409 kg/ha and G*ge*=443 kg/ha during *kharif*. Similarly, another variety TG-37A having higher yield performance with higher G*ge* coupled with high G*g* values during spring has been released for commercial cultivation in 2019.

In plant breeding, Multi-Environment Trials (MET) are important as it allows the evaluation of genotype(s) under different environmental condition, which enables to assess and compare their response, overall stability and adaptation. Thus, best genotype(s) can be selected for a specific environment and across environments for further testing, but it is not easy because of the presence of Genotype by Environment Interaction (GEI). For sustainable agricultural system the adaptability of genotype(s) is of paramount importance for marginal farmers, as low GEI gives assurance for more guaranteed yield in the targeted environment. In the absence of GEI, means across environments can be used as indicator, however, in the presence of GEI, the use of means across environments ignores the fact that genotypes differ in their relative performance over environments (Voltas *et al*., 2002). In such situation, if genotype and environment means are used to predict the yield potential of the recommended cultivar(s), it will cause a failure of formal breeding to serve small resource-poor farmers in marginal fragile environments (Ceccarelli *et al*., 2006).

In Punjab, groundnut is mainly grown during the *kharif* season in an area of 1.3 thousand hectares (2018-19) but the prevailing cropping pattern of paddy-wheat is diverting some acreage to potato, green pea and other vegetable crops in spring season as these climatic conditions are favourable for high groundnut productivity, therefore characterization of germplasm for spring and *kharif* season is crucial to get maximum pod yield potential of groundnut as a third crop in paddy-green pea/another vegetable-spring groundnut pattern. The significant differential response of genotypes across the seasons, as implied by crossover interaction, recommended the evaluation of advance breeding lines in the target environment for variety testing for release of stable and adapted varieties to particular ecologies. The selection of candidature genotype(s) solely on the basis of phenotypic value will be misleading. Hence, the selection should be emphasised on genotypic values and its interaction with the environment. The conventional phenotypic values in the present study are sum of the fixed effects and BLUP genotypic values. BLUP serve as a great tool to select best individuals as it maximizes the correlation of true genotypic values and the predicted genotypic values (Searle *et al*., 1992). The partitioning of BLUP genotypic values specifies the contribution of genotypic value (*Gg*) and environmental effects (G*ge*) to the yield potential of the genotype. The change in the ranking of genotypes with respect to G*g* and G*gge* values indicates the differential response of genotype(s) across the seasons. These observations based on the ranking of genetic values are in agreement with the findings of Smith and Cullis (2018) and Crossa *et al*. (2006) as they have suggested that the random modelling gives more precise estimate of the genetic values. All the genotypes were found to have high BLUP genotypic values, which on partitioning showed the significant contribution of environment to the overall performance of the genotype, coupled with high genetic values. All the genotypes were found to have high genetic values along with moderate to high G*ge* value during the spring season, than during the *kharif* season in which they had low G*ge* value. Thus, the genotypes were found to be specifically adapted to spring season. Hu (2015) compared two statistical methods for analysing rape cultivar multilocation trials: separate ANOVA and BLUP. He found that BLUP provided more accurate and efficient predictions of location-specific genotype effects compared to separate ANOVA. The Pearson correlation of genotype prediction between locations was higher for BLUP and the average variance of differences between genotype estimates was lower for BLUP. These results suggest that BLUP is a more effective method for analyzing rape cultivar in multilocation trials which corresponds to the result of current study.

CONCLUSION

The results of the study indicated that the high G*g* values of genotypes is alone not a capable factor for the commercialization as, G*ge* is the deciding factor for the adaptability to the targeted region. Hence, the selection should be emphasized on the high G*g* value coupled with low G*ge* value for wide adaptability or high G*g* with high G*ge* for specific season to harvest maximum yield potential of the genotype. This will ensure the optimum productivity for small scale farmers.

Conflict of interest

All authors declare that they have no conflicts of interest.

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